

SEQUENCE LISTING

<110> Duvick, Jon

<120> Compositions and Methods for Fummonisin Detoxification

<130> 5718-111

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<170> PatentIn Ver. 2.0

<210> 1

<211> 1691

<212> DNA

<213> *Exophiala spinifera*

<220>

<223> flavin monooxygenase with intron

<400> 1

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<211> 1638

<212> DNA

<213> *Exophiala spinifera*

<220>

<223> flavin monooxygenase, fully spliced cDNA

<400> 2

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<210> 3

<211> 545

<212> PRT

<213> *Exophiala spinifera*

<220>

<223> flavin monooxygenase, translation of fully spliced
cDNA

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Ala Ile Ile Val Gly Ala Gly Leu Ser Gly Ile Ser Ala Val Tyr Lys
20 25 30

Leu Arg Lys Leu Arg Leu Asn Ala Lys Ile Phe Glu Gly Ala Pro Asp
35 40 45

Phe Gly Gly Val Trp His Trp Asn Arg Tyr Pro Gly Ala Arg Val Asp
50 55 60

Ser Glu Thr Pro Phe Tyr Gln Leu Asn Ile Pro Glu Val Trp Lys Asp
65 70 75 80

Trp Thr Trp Ser Cys Arg Tyr Pro Asp Gln Lys Glu Leu Leu Ser Tyr
85 90 95

Val His His Cys Asp Lys Ile Arg Gly Leu Arg Lys Asp Val Tyr Phe
100 105 110

Gly Ala Glu Val Val Asp Ala Arg Tyr Ala Arg Asp Leu Gly Thr Trp
115 120 125

Thr Val Lys Thr Ser Ala Gly His Val Ala Thr Ala Lys Tyr Leu Ile
130 135 140

Leu Ala Thr Gly Leu Leu His Arg Lys His Thr Pro Ala Leu Pro Gly
145 150 155 160

Leu Ala Asp Phe Asn Gly Lys Val Ile His Ser Ser Ala Trp His Glu
165 170 175

Asp Phe Asp Ala Glu Gly Gln Arg Val Ala Val Ile Gly Ala Gly Ala
180 185 190

Thr Ser Ile Gln Ile Val Gln Glu Leu Ala Lys Lys Ala Asp Gln Val
195 200 205

Thr Met Phe Met Arg Arg Pro Ser Tyr Cys Leu Pro Met Arg Gln Arg
210 215 220

Thr	Met	Asp	Arg	Asn	Glu	Gln	Thr	Ala	Trp	Lys	Ala	Tyr	Tyr	Pro	Thr	225	230	235	240
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Pro	Ser	Val	Gly	Ile	Phe	Glu	Val	Ser	Pro	Glu	Gln	Arg	Glu	Ala	Tyr	260	265	270	
Phe	Glu	Glu	Leu	Trp	Glu	Arg	Gly	Ala	Phe	Asn	Phe	Leu	Ala	Cys	Gln	275	280	285	
Tyr	Arg	Glu	Val	Met	Val	Asp	Lys	Lys	Ala	Asn	Arg	Leu	Val	Tyr	Asp	290	295	300	
Phe	Trp	Ala	Lys	Lys	Thr	Arg	Ser	Arg	Ile	Val	Asn	Pro	Ala	Lys	Arg	305	310	315	320
Asp	Leu	Met	Ala	Pro	Leu	Glu	Pro	Pro	Tyr	Trp	Phe	Gly	Thr	Lys	Arg	325	330	335	
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Leu	Lys	Asn	Lys	His	Gly	Val	Asp	Leu	Lys	Glu	Val	Trp	Lys	Asp	Gly	405	410	415	
Ile	Ser	Thr	Tyr	Met	Gly	Val	Phe	Ser	His	Gly	Phe	Pro	Asn	Ala	Phe	420	425	430	
Phe	Val	Ala	Thr	Ala	Gln	Ala	Pro	Thr	Val	Leu	Ser	Asn	Gly	Pro	Thr	435	440	445	
Ile	Ile	Glu	Thr	Gln	Val	Asp	Leu	Ile	Ala	Asp	Thr	Ile	Ala	Lys	Leu	450	455	460	
Glu	Ala	Glu	His	Ala	Thr	Ser	Val	Glu	Ala	Thr	Lys	Ser	Ala	Gln	Glu	465	470	475	480

Ala Trp Ser Ile Met Ile Ala Lys Met Asn Glu His Thr Leu Phe Pro
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Leu Thr Asp Ser Trp Trp Thr Gly Gly Asn Ile Pro Gly Lys Ala Thr
500 505 510

Arg Ala Leu Thr Phe Ile Gly Gly Ile Ala Leu Tyr Glu Gln Ile Cys
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Gln Glu Lys Val Ala Asn Trp Asp Gly Phe Asp Val Leu His Ala Pro
530 535 540

Cys
545

<210> 4

<211> 1464

<212> DNA

<213> *Exophiala spinifera*

<220>

<223> aldehyde dehydrogenase , fully spliced cDNA

<400> 4

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<210> 5

<211> 487

<212> PRT

<213> *Exophiala spinifera*

<220>

<223> aldehyde dehydrogenase, translation of fully
spliced cDNA

<400> 5

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35 40 45

Asp Val Asp Ser Ala Val Ala Ala Ser Val Gln Ala Val Lys Lys Gly
50 55 60

Pro Trp Lys Lys Phe Thr Gly Ala Gln Arg Ala Ala Cys Met Leu Lys
65 70 75 80

Phe Ala Asp Leu Ala Glu Lys Asn Ala Glu Lys Leu Ala Arg Leu Glu
85 90 95

Ser Leu Pro Thr Gly Arg Pro Val Ser Met Ile Thr His Phe Asp Ile
100 105 110

Pro Asn Met Val Ser Val Phe Arg Tyr Tyr Ala Gly Trp Ala Asp Lys
115 120 125

Ile Ala Gly Lys Thr Phe Pro Glu Asp Asn Gly Lys Pro Asn Trp Arg
130 135 140

Tyr Glu Pro Met Gly Val Cys Ala Gly Ile Ala Ser Trp Asn Ala Thr
145 150 155 160

Phe Leu Tyr Val Gly Trp Lys Ile Ala Pro Ala Leu Ala Ala Gly Cys
165 170 175

Ser Phe Ile Phe Lys Ala Ser Glu Lys Ser Pro Leu Gly Val Leu Gly
180 185 190

Leu Ala Pro Leu Phe Ala Glu Ala Gly Phe Pro Pro Gly Val Val Gln
 195 200 205

Phe Leu Thr Gly Ala Arg Val Thr Gly Glu Ala Leu Ala Ser His Met
 210 215 220

Asp Ile Ala Lys Ile Ser Phe Thr Arg Ser Val Gly Gly Gly Arg Ala
 225 230 235 240

Val Lys Gln Ala Thr Leu Lys Ser Asn Met Lys Arg Val Thr Leu Glu
 245 250 255

Leu Gly Glu Lys Pro Thr Ile Val Phe Asn Glu Ala Pro Leu Glu Arg
 260 265 270

Gln Ser Gly Glu Ser Ala Lys Asp Phe Ser Lys Phe Gly Gln Ile Trp
 275 280 285

Val Pro Pro Ser Cys Leu Leu Val Gln Trp Gly Asn Leu Ala Glu Lys
 290 295 300

Phe His Gly Val Arg His Gly Ser Phe Gly Gly Cys Gln Arg Trp Leu
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Gly Gln Asn Pro Leu Glu Pro Lys Arg Thr His Gly Pro Phe Val Asp
 325 330 335

Lys Ser Gln Tyr Asp Arg Val Leu Gly Asn Ile Asp Val Gly Lys Asp
 340 345 350

Thr Ala Gln Leu Leu Thr Gly Val Gly Arg Lys Gly Asp Lys Gly Phe
 355 360 365

Ala Ile Glu Pro Thr Ile Phe Val Asn Pro Lys Pro Gly Ser Lys Ile
 370 375 380

Trp Phe Glu Glu Ile Phe Gly Pro Val Leu Ser Ile Lys Thr Phe Lys
 385 390 395 400

Thr Glu Glu Glu Ala Ile Glu Ile Ala Asn Asp Thr Thr Tyr Gly Leu
 405 410 415

Ala Ser Val Ile Tyr Thr Lys Ser Leu Asn Arg Gly Leu Arg Val Ser
 420 425 430

Ser Ala Leu Glu Thr Gly Gly Val Ser Ile Asn Phe Pro Phe Ile Pro
 435 440 445

Glu Thr Gln Thr Pro Phe Gly Gly Met Lys Gln Ser Gly Ser Gly Arg
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Glu Leu Gly Glu Glu Gly Leu Lys Ala Tyr Leu Glu Pro Lys Thr Ile
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Asn Ile His Val Asn Ile Glu
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<210> 6

<211> 1764

<212> DNA

<213> *Exophiala spinifera*

<220>

<223> permease, partially spliced cDNA

<400> 6

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<210> 7

<211> 1578

<212> DNA

<213> *Exophiala spinifera*

<220>

<223> permease, fully spliced cDNA

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<210> 8

<211> 525

<212> PRT

<213> *Exophiala spinifera*

<220>

<223> permease, translation of fully spliced cDNA

<400> 8

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20 25 30

Leu Asn Val Pro Leu Glu Lys Lys Gln Phe Gly Thr Ile Thr Ile Val
35 40 45

Ser Leu Ala Phe Val Ile Cys Asn Ser Trp Ala Gly Ile Ser Gly Ser
50 55 60

Leu Gln Leu Ala Leu Leu Ala Gly Gly Pro Val Thr Leu Leu Tyr Gly
65 70 75 80

Ile Leu Ile Ser Thr Leu Val Tyr Ile Cys Ile Ala Phe Ser Leu Ala
85 90 95

Glu Leu Thr Ser Val Tyr Pro Thr Ala Gly Gly Gln Tyr His Phe Ala
100 105 110

Ser Ile Leu Ala Pro Lys Ser Ile Asn Arg Ser Ile Ser Tyr Val Cys
115 120 125

Gly Leu Val Ser Leu Leu Ser Trp Ile Ala Ile Gly Ser Ser Val Thr
130 135 140

Met Ile Pro Ala Gln Gln Ile Pro Ala Leu Ile Ala Ala Tyr Ser His
145 150 155 160

Thr Tyr Ser Gln Asp Ser Trp His Val Phe Leu Ile Tyr Glu Gly Val
165 170 175

Ala Leu Val Val Leu Leu Phe Asn Leu Phe Ala Leu Lys Arg Asn Pro
180 185 190

Trp Val His Glu Ile Gly Phe Gly Leu Thr Ile Ala Leu Phe Val Ile
195 200 205

Ser Phe Ile Ala Ile Leu Ala Arg Ser Asn Pro Lys Ala Pro Asn Ser
210 215 220

Gln Val Trp Thr Ala Trp Ser Asn Tyr Thr Gly Trp Ser Asp Gly Val
225 230 235 240

Cys Phe Ile Leu Gly Leu Ser Thr Ser Cys Phe Met Phe Ile Gly Leu
245 250 255

Asp Ala Ala Met His Leu Ala Glu Glu Cys Thr Asp Ala Ala Arg Thr
 260 265 270

Val Pro Lys Ala Val Val Ser Ala Ile Ile Ile Gly Phe Cys Thr Ala
 275 280 285

Phe Pro Tyr Thr Ile Ala Val Leu Tyr Gly Ile Thr Asp Leu Asp Ser
 290 295 300

Ile Leu Ser Ser Ala Gly Tyr Ile Pro Phe Glu Thr Met Arg Gln Ser
 305 310 315 320

Ala Arg Ile Arg Leu Phe Ala Thr Val Leu Ser Cys Gly Gly Ile Val
 325 330 335

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 340 345 350

Thr Trp Ser Phe Ala Arg Asp Asn Gly Leu Val Phe Ser Thr His Leu
 355 360 365

Glu Arg Ile His Pro Arg Trp Gln Val Pro Val Trp Ser Leu Phe Ala
 370 375 380

Thr Trp Gly Ile Leu Ala Thr Cys Gly Cys Ile Phe Leu Gly Ser Ser
 385 390 395 400

Thr Ala Phe Asn Ala Leu Val Asn Ser Ala Val Val Leu Gln Gln Leu
 405 410 415

Ser Phe Leu Ile Pro Ile Ala Leu Leu Leu Tyr Gln Lys Arg Asp Pro
 420 425 430

Lys Phe Leu Pro Ser Thr Arg Ala Phe Val Leu Pro Arg Gly Ile Gly
 435 440 445

Phe Leu Val Asn Val Leu Ala Val Val Phe Thr Ser Val Thr Thr Val
 450 455 460

Phe Phe Ser Phe Pro Leu Thr Val Pro Thr Ala Ala Ser Thr Met Asn
 465 470 475 480

Tyr Thr Ser Ala Ile Ile Gly Val Ala Leu Ala Leu Gly Val Leu Asn
 485 490 495

Trp Val Val His Ala Arg Lys His Tyr Gln Gly Pro His Leu Glu Leu
 500 505 510

Asp Gly Arg Val Val Gly Ala Glu Phe Gln Val Gly Pro
515 520 525

<210> 9

<211> 3999

<212> DNA

<213> *Exophiala spinifera*

<220>

<223> p-glycoprotein, with introns

<400> 9

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 gacaatagca gtggcgcacc gactttccac tattcggaat gttgatgtta tttttgtgtt 3720
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 gaaaagggcg gtgggatctt ttaggatagg tttagtggcg tggtacttac tacaggcggt 3900
 tggattcagg tacgacaact tgtacaataa gtagcataga gcatgtaatg aaagggtact 3960
 cgtcccggaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3999

<210> 10

<211> 3792

<212> DNA

<213> *Exophiala spinifera*

<220>

<223> p-glycoprotein, fully spliced cDNA

<400> 10

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 gccgacaaat acgactggac tctcaatgtc atcgcgctca tctgcgccat cggatccggg 180
 gcttcccttc ctctgatgtc gatcatcttc ggtagcttca ccaacaagtt caacaattac 240
 aattcggggcg acgggagtc tgaagcggtc aaggccgatg tggatcattt cgtcctgtgg 300

tcaacgttga tcgctttgtc ggaacgattc tacgacccga cctcgggccg aatttcattt 3240
gcacacgaga atattgcaga aatgtcgccg cgcttgtacc gcggccatat gtctttggtc 3300
caacaggaac ccacacttta ccaaggctcc gttcgcgaga atgtgacgtt ggccctcgaa 3360
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tccggcgggc aacgacagcg gatcgccatc gcaagagcat tgattcgaaa tccaaagctg 3540
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gccctcgatg aggcattcac gagccgaacg acaatagcag tggcgcaccg actttccact 3660
attcggaatg ttgatgttat ttttgtgttt gccaacggga gaatcgccga aacgggcact 3720
cacgcggaac tacaacgact gagaggaaga tattacgaga tgtgtttggc acaatcttta 3780
gaccaagcat ga 3792

<210> 11

<211> 1263

<212> PRT

<213> *Exophiala spinifera*

<220>

<223> p-glycoprotein, translation of fully spliced cDNA

<400> 11

Met Ala Asp Glu Ser Glu Lys Pro Arg Pro Asn Gln Asp Gly Ser Glu
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Ser Ser Ser His Pro Pro Pro Glu Lys Glu Thr Glu Gly Ser Ile Ser
20 25 30

Asp Tyr Leu Arg Ile Phe Arg Tyr Ala Asp Lys Tyr Asp Trp Thr Leu
35 40 45

Asn Val Ile Ala Leu Ile Cys Ala Ile Gly Ser Gly Ala Ser Leu Pro
50 55 60

Leu Met Ser Ile Ile Phe Gly Ser Phe Thr Asn Lys Phe Asn Asn Tyr
65 70 75 80

Asn Ser Gly Asp Gly Ser Pro Glu Ala Phe Lys Ala Asp Val Asp His
85 90 95

Phe Val Leu Trp Phe Val Tyr Leu Phe Ile Gly Lys Phe Val Leu Thr
100 105 110

Tyr Val Ser Thr Ala Ala Ile Thr Ile Ser Ala Ile Arg Thr Thr Arg
115 120 125

Thr Leu Arg Arg Val Phe Leu Glu Cys Thr Leu Arg Gln Glu Val Trp
130 135 140

His Phe Asp Lys Gln Ser Asn Gly Ala Ile Ala Thr Xaa Val Thr Thr
 145 150 155 160

Asn Gly Asn Arg Ile Gln Thr Gly Ile Ala Glu Lys Leu Val Phe Thr
 165 170 175

Val Gln Ala Leu Ser Met Phe Phe Ser Ala Phe Val Val Ala Leu Ala
 180 185 190

Ser Gln Trp Lys Leu Ala Leu Ile Thr Met Ser Val Ile Pro Ala Ile
 195 200 205

Phe Leu Val Thr Gly Ile Cys Ile Ala Ile Asp Ala Ala Gln Glu Ala
 210 215 220

Arg Ile Thr Arg Ile Tyr Ser Arg Ala Ala Val Leu Ala Glu Glu Val
 225 230 235 240

Leu Ser Ser Ile Arg Thr Val His Ala Phe Tyr Ala Gln Lys Lys Met
 245 250 255

Val Glu Lys Tyr Asp Val Phe Leu Gln Gln Ala His Gln Glu Gly Lys
 260 265 270

Lys Lys Ser Pro Asn Asn Gly Val Leu Phe Ser Thr Glu Tyr Phe Cys
 275 280 285

Ile Tyr Ala Ala Ile Ala Leu Ala Phe Trp Lys Gly Phe Arg Met Tyr
 290 295 300

Gln Asn Gly Glu Val Ala Asp Val Gly Lys Val Phe Thr Val Val Leu
 305 310 315 320

Ser Val Thr Leu Ala Ala Thr Ser Ile Ser Met Leu Ala Pro Ser Gly
 325 330 335

Ser Val Val Tyr Gln Arg Arg Ile Phe Gly Ser Glu Leu Phe Ser Ile
 340 345 350

Ile Asp Lys Pro Thr Gln Leu Asp Pro Leu Asp Pro Ser Gly Lys Gln
 355 360 365

Pro Glu Gly Cys Leu Gly Gln Ile Glu Ile Gln Asn Leu Ala Phe Ala
 370 375 380

Tyr Pro Ser Arg Pro Ser Ala Gln Val Leu Arg Asp Phe Asn Leu Thr
 385 390 395 400

Ile Pro Ala Gly Lys Thr Thr Ala Leu Val Gly Ala Ser Gly Ser Gly
 405 410 415

Lys Ser Thr Met Val Gly Leu Leu Glu Arg Trp Tyr Leu Pro Ser Ser
 420 425 430

Gly Arg Ile Leu Leu Asp Gly Leu Glu Leu Gly Gln Tyr Asn Val Lys
 435 440 445

Trp Leu Arg Ser Arg Ile Arg Leu Val Gln Gln Glu Pro Val Leu Phe
 450 455 460

Arg Gly Thr Ile Phe Gln Asn Ile Ala Asn Gly Phe Met Asp Glu Gln
 465 470 475 480

Arg Asp Leu Pro Arg Glu Lys Gln Met Glu Leu Val Gln Lys Ala Cys
 485 490 495

Lys Ala Ser Asn Gly Asp Val Phe Ile Asn Glu Leu Pro Asn Gly Tyr
 500 505 510

Glu Thr Glu Val Gly Glu Arg Ala Gly Ala Leu Ser Gly Gly Gln Arg
 515 520 525

Gln Arg Ile Ala Ile Ala Arg Ser Ile Ile Ser Asp Pro Lys Ile Leu
 530 535 540

Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp Pro Lys Ala Glu Lys Val
 545 550 555 560

Val Gln Glu Ala Leu Asn Arg Val Ser Lys Asp Arg Thr Thr Leu Val
 565 570 575

Ile Ala His Lys Leu Ala Thr Val Lys Ser Ala Gly Asn Ile Ala Val
 580 585 590

Ile Ser Gln Gly Lys Ile Val Glu Gln Gly Thr His His Glu Leu Ile
 595 600 605

Glu Phe Gly Cys His Tyr Ala Ala Leu Val Arg Ala Gln Asp Leu Gly
 610 615 620

Ala Asp Glu Gln Gln Glu His Glu Lys Thr Leu His Glu Lys Ala Ala
 625 630 635 640

Arg Glu Ala Ala Gly Glu Arg Pro Ala Leu Glu Arg Thr His Thr Thr
 645 650 655

Ala Thr Ser Gln Ala Gly Asp Leu Glu Lys Arg Lys Val Pro Val Gly
660 665 670

Thr Leu Gly Tyr Ser Leu Leu Lys Cys Ile Leu Ile Met Phe Tyr Glu
675 680 685

Gln Lys Asn Leu Tyr Trp Cys Phe Leu Leu Ser Thr Ile Thr Val Leu
690 695 700

Ile Cys Ala Ala Thr Phe Pro Gly Gln Ala Leu Leu Phe Ser Arg Leu
705 710 715 720

Leu Thr Val Phe Glu Leu Ser Gly His Ala Ala Gln Glu Arg Ala Asp
725 730 735

Phe Tyr Ile Leu Met Phe Phe Val Val Ala Leu Gly Asn Leu Val Gly
740 745 750

Tyr Phe Thr Ile Gly Trp Thr Cys Asn Val Ile Ser Gln Val Val Thr
755 760 765

His Arg Tyr Gln Ala Ala Met Phe Gln Arg Val Leu Asp Gln Asp Ile
770 775 780

Glu Leu Leu Asp Ile Pro Glu Gln Ile Ser Gly Ala Leu Thr Ser Gln
785 790 795 800

Leu Ser Ala Leu Pro Thr Gln Leu Gln Glu Leu Ile Ser Ala Asn Phe
805 810 815

Leu Ile Tyr Ile Val Val Gly Gln His Arg Leu Glu Gln Cys Ser Thr
820 825 830

Thr Ser Leu Trp Met Glu Thr Gly Pro Gly Gly Cys Val Trp Cys Thr
835 840 845

Ser Thr Pro Ala Phe Gly Trp Leu Pro Gln Asn Ser Ser Arg Asp Glu
850 855 860

Ala Arg Ser Arg Lys Leu Gly Lys Leu Cys Arg Lys Cys Trp Ala Cys
865 870 875 880

Lys Arg Ser Ser Tyr Arg Asp Pro Asp Arg Leu Ile Phe Asp Ser Arg
885 890 895

Arg Pro Cys Ser Pro Thr Val Leu Gly His Val Glu Gln Gly Leu Ala
900 905 910

Lys Ile Ile Gln Ser Phe Trp Phe Gly Arg Cys Phe Gly Phe His Leu
915 920 925

Ser Gln Ser Met Glu Phe Leu Ala Ile Ala Leu Gly Phe Cys Ile Ala
930 935 940

Val Asp Asn Trp Leu Gln Val Ser Thr Thr Gln Leu Asn Phe Ile Ser
945 950 955 960

Ser Ser Trp Ala Phe Cys Leu Pro Val Gln Ala Ala Ala Gln Tyr Leu
965 970 975

Ala Tyr Ser Thr Ser Phe Thr Lys Ala Arg Ser Ala Ala Asn Tyr Ile
980 985 990

Leu Trp Leu Arg Thr Leu Lys Pro Thr Ile Arg Glu Thr Glu Glu Asn
995 1000 1005

Lys Lys Lys Gly Pro Val Gly Gly Cys Pro Val Asp Leu Glu Asp Ile
1010 1015 1020

Glu Phe Arg Tyr Arg Gln Arg Asp Ser Ala Arg Val Leu Arg Gly Val
1025 1030 1035 1040

Ser Met Thr Ile Glu Pro Gly Gln Phe Val Ala Tyr Val Gly Ala Ser
1045 1050 1055

Gly Cys Gly Lys Ser Thr Leu Ile Ala Leu Ser Glu Arg Phe Tyr Asp
1060 1065 1070

Pro Thr Ser Gly Arg Ile Ser Phe Ala His Glu Asn Ile Ala Glu Met
1075 1080 1085

Ser Pro Arg Leu Tyr Arg Gly His Met Ser Leu Val Gln Gln Glu Pro
1090 1095 1100

Thr Leu Tyr Gln Gly Ser Val Arg Glu Asn Val Thr Leu Ala Leu Glu
1105 1110 1115 1120

Ala Glu Leu Ser Glu Glu Leu Cys Gln Gly Arg Leu Pro Ala Arg Pro
1125 1130 1135

Met Leu Trp Ile Leu Ser Ser Leu Tyr Gln Lys Ala Leu Lys Arg Leu
1140 1145 1150

Ala Ala Gln Arg Gly Met Gln Phe Ser Gly Gly Gln Arg Gln Arg Ile
1155 1160 1165

Ala Ile Ala Arg Ala Leu Ile Arg Asn Pro Lys Leu Leu Leu Leu Asp
1170 1175 1180

Glu Ala Thr Ser Ala Leu Asp Thr Gln Ser Glu Arg Leu Val Gln Ala
1185 1190 1195 1200

Ala Leu Asp Glu Ala Ser Thr Ser Arg Thr Thr Ile Ala Val Ala His
1205 1210 1215

Arg Leu Ser Thr Ile Arg Asn Val Asp Val Ile Phe Val Phe Ala Asn
1220 1225 1230

Gly Arg Ile Ala Glu Thr Gly Thr His Ala Glu Leu Gln Arg Leu Arg
1235 1240 1245

Gly Arg Tyr Tyr Glu Met Cys Leu Ala Gln Ser Leu Asp Gln Ala
1250 1255 1260